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SEQUENCE LISTING

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<120> MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS

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tggctctccc gtcccctgga gaagaacaag gcc atg ggt cgg ccc ctg ctg ctg 174
Met Gly Arg Pro Leu Leu Leu
-19 -15

ccc cta ctg ccc ctg ctg ctg ccg cca gca ttt ctg cag cct agt ggc 222
Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly
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tcc aca gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa 270
Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys
5 10 15 20

cac ctc tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc 318
His Leu Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe
25 30 35

tat tac ccc tgg gag tta gcc aca gct ccc gac gtg aga ata tcc tgg 366
Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp
40 45 50

tcc att cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag 462
Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu
70 75 80

cag tct gtg tat ttc tgc cga gtt gag ctg gac aca cgg agc tca ggg 558
Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly
105 110 115

gct gtc acg acc acc acc cag agg ccc agc agc atg act acc acc tgg 654
Ala Val Thr Thr Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Thr Trp
135 140 145

aaa cga cgc tca gac tct tgg cac ata agt ctg gag act gct gtg ggg 750
Lys Arg Arg Ser Asp Ser Trp His Ile Ser Leu Glu Thr Ala Val Gly
165 170 175 180

tgc	ctc	ctc	agg	tgg	agg	aga	agg	aaa	ggt	cag	cag	cgg	act	aaa	gcc	846
Cys	Leu	Leu	Arg	Trp	Arg	Arg	Arg	Lys	Gly	Gln	Gln	Arg	Thr	Lys	Ala	
			200					205					210			

aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag 942
Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys
230 235 240

ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac gag 1038
 Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu
 265 270 275

acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa 1092
 Thr Leu Tyr Ser Val Leu Lys Ala
 280

tggtgaggcc aggtacagtg gcgcacacct gtaatcccag ctactctgaa gcctgaggca 1152

gaatcaagtg agcccaggag ttcagggcca gctttgataa tggagcgaga tgccatctct 1212

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Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
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 30 35 40 45

Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
 50 55 60

Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
 65 70 75

Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
 80 85 90

Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
 95 100 105

Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
 110 115 120 125

Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Thr Gln Arg Pro
 130 135 140

Ser Ser Met Thr Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr Thr
 145 150 155

Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile
 160 165 170

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Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly
 175 180 185

Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
 190 195 200 205

Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
 210 215 220

Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
 225 230 235

Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
 240 245 250

Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro
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 Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro
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agc tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg 264
 Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met
 15 20 25

ggt ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta 312
 Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu
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gcc aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac 360
 Ala Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His
 45 50 55 60

ggg cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat 408
 Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr
 65 70 75

gtg aac cgg ctg ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc 456
 Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe
 80 85 90

ctc agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc 504
 Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys
 95 100 105

cga gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc 552
 Arg Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser
 110 115 120

atc gag ggg acc aaa ctg tcc atc acc cag ggt cag cag cgg act aaa 600
 Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys
 125 130 135 140

gcc aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat 648
 Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr
 145 150 155

gag aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc 696
 Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro
 160 165 170

aag gat gac ggc atc gtc tat gct tcc ctt gcc ctg tcc agc tcc acc 744
 Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr
 175 180 185

tca ccc aga gca cct ccc agc cac cgt ccc ctg aag agc ccc cag aac 792
 Ser Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn
 190 195 200

gag acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct 839
 Glu Thr Leu Tyr Ser Val Leu Lys Ala
 205 210

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Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
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Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
35 40 45

Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
50 55 60

Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
65 70 75

Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
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Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
100 105 110

Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
115 120 125

Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys Ala Thr Thr
130 135 140

Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu Asn Ile
145 150 155

Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys Asp Asp
160 165 170 175

Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser Pro Arg
180 185 190

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cagacatctg tgcctcattc ctgatctcaa ggggaaagca agaacaaggg aggcttcctc 180
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atacagatca gggaggctgt cgtggcagtc catcaagggg acccacctca ccatcaccca 300
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ccgtcccttg gagaagaaca aggcc atg ggt cgg ccc ctg ctg ctg ccc ctg 412
Met Gly Arg Pro Leu Leu Leu Pro Leu
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Leu Leu Leu Leu Gln Pro Pro Ala Phe Leu Gln Pro Gly Gly Ser Thr
-5 1 5
gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa cac ctc 508
Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu
10 15 20
tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc tat tac 556
Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr
25 30 35 40
ccc tgg gag tta gcc ata gtt ccc aac gtg aga ata tcc tgg aga cgg 604
Pro Trp Glu Leu Ala Ile Val Pro Asn Val Arg Ile Ser Trp Arg Arg
45 50 55
ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct tcc att 652
Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile
60 65 70
cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag ggt cag 700
His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln
75 80 85
gag agc ggc ttc ctc agg atc tca aac ctg cgg aag gag gac cag tct 748
Glu Ser Gly Phe Leu Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser
90 95 100
gtg tat ttc tgc cga gtc gag ctg gac acc cgg aga tca ggg agg cag 796
Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln
105 110 115 120

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 Gln Leu Gln Ser Ile Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val
 125 130 135

aca acc acc acc acc tgg agg ccc agc agc aca acc acc ata gcc ggc 892
 Thr Thr Thr Thr Thr Trp Arg Pro Ser Ser Thr Thr Thr Ile Ala Gly
 140 145 150

ctc agg gtc aca gaa agc aaa ggg cac tca gaa tca tgg cac cta agt 940
 Leu Arg Val Thr Glu Ser Lys Gly His Ser Glu Ser Trp His Leu Ser
 155 160 165

ctg gac act gcc atc agg gtt gca ttg gct gtc gct gtg ctc aaa act 988
 Leu Asp Thr Ala Ile Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr
 170 175 180

gtc att ttg gga ctg ctg tgc ctc ctc ctc ctg tgg tgg agg aga agg 1036
 Val Ile Leu Gly Leu Leu Cys Leu Leu Leu Leu Trp Trp Arg Arg Arg
 185 190 195 200

aaa ggt agc agg gcg cca agc agt gac ttc tgaccaacag agtgtgggga 1086
 Lys Gly Ser Arg Ala Pro Ser Ser Asp Phe
 205 210

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gcaaggcaga aggaggctgg gtccctgaat caccgactgg aggagagtta cctacaagag 1266

ccttcatcca ggagcatcca cactgcaatg atataggaat gaggtctgaa ctccactgaa 1326

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Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
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Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Ile Val
 35 40 45

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Pro Asn Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
50 55 60

Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
65 70 75

Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile
80 85 90 95

Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
100 , 105 110

Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly
115 120 125

Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr Trp Arg
130 135 140

Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys
145 150 155

Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
160 165 170 175

Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
180 185 190

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aacaaggcc atg ggt cgg ccc ctg ctg ctg ccc cta ctg ccc ctg ctg ctg 171

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 Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser
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 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
 15 20 25

ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta gcc 315
 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
 30 35 40 45

aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 363
 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
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cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg 411
 Gln Ser Phe Tyr Ser Thr Arg Pro Ser Ile His Lys Asp Tyr Val
 65 70 75

aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc ctc 459
 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
 80 85 90

agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc cga 507
 Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg
 95 100 105

gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc atc 555
 Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile
 110 115 120 125

gag ggg acc aaa ctc tcc atc acc cag ggg aac cct tcc aaa aca cag 603
 Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Asn Pro Ser Lys Thr Gln
 130 135 140

agg agc cat atg aga ata tca gga atg aag gac aaa ata cag atc cca 651
 Arg Ser His Met Arg Ile Ser Gly Met Lys Asp Lys Ile Gln Ile Pro
 145 150 155

agc taa atcccaagga tgacggcatc gtctatgctt cccttgccct ctccagctcc 707
 Ser

acctcaccca gagcacctcc cagccaccgt cccctcaaga gccccagaa cgagaccctg 767

tactctgtct taaaggccta accaatggac agccctctca agactgaatg gtgaggccag 827

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Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
15 20 25

Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
30 35 40 45

Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
50 55 60

Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
65 70 75

Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
80 85 90

Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg
95 100 105

Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile
110 115 120 125

Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Asn Pro Ser Lys Thr Gln
130 135 140

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atggagagca cctgaggac ctttaaaagg caaagccgca aggcagaagg aggctgggtc 1149

cctgaatcac cgactggagg agagttacct acaagagcct tcatccagga gcatccacac 1209

tgcaatgata taggaatgag gtctgaactc cactgaatta aaccactggc atttgggggc 1269

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-1 1 5 10

Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
15 20 25

Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
30 35 40 45

Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
50 55 60

Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
65 70 75

Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu
80 85 90

